

## SEQUENCE LISTING

<110> Ziv , Shani  
Shoseyov, Oded

<120> PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECOMBINANT  
PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTURED PLANT CELLS

<130> 01/22924

<160> 26

<170> PatentIn version 3.1

<210> 1

<211> 4

<212> PRT

<213> Unknown

<220>

<223> ER retaining signal peptide

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His Asp Glu Leu  
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<210> 2

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<213> Unknown

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Lys Asp Glu Leu  
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<210> 3

<211> 150

<212> DNA

<213> *Arabidopsis thaliana*

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<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

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<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 5

aaaatctaga ttacggaga gcgtcgcg 28

<210> 6

<211> 1305

<212> DNA

<213> Artificial sequence

<220>

<223> ProtL-CBDcex DNA construct

<400> 6

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tcaaaggaac atttgaaaaa gcaacatcag aagcttatga gtatgcagat actttgaaga 180  
aagacaatgg agaataact gtatgtgtg cagataaagg ttatacttta aatattaaat 240  
ttgctggaaa agaaaaaaca ccagaagaac caaaagaaga agttactatt aaagcaaact 300

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taatctatgc agatggaaaa acacaaacag cagaattcaa aggaacattt gaagaagcaa 360
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<211> 32

<212> DNA

<213> Artificial sequence

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<223> Single strand DNA oligonucleotide

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<210> 8

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 8

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aaaagtcgac ttaaagttca tcatgctcga cgccgaccgt gca 43

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<210> 9

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 9

aaaaactagt gctagcggtc cagccggc

28

<210> 10

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 10

aaaagtcgac ttaaagttca tcatgtccaa cggtgcaagg ggc

43

<210> 11

<211> 1418

<212> DNA

<213> Artificial sequence

<220>

<223> pUC19-cell1-ProtL-cexNG-HDEL fusion construct

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tctctccgcc gatttactcc gccggtcacg attaccgcga cgctctccgt aaatctagaa

120

tggcggcgggt agaaaataaa gaagaaacac cagaaacacc agaaactgat tcagaagaag

180

aagtaacaat caaagctaac ctaatctttg caaatggaag cacacaaact gcagaattca

240

aaggaacatt tgaaaaagca acatcagaag cttatgagta tgcagatact ttgaagaaag

300

acaatggaga atatactgta gatgttgag ataaaggta tactttaaat attaaatttg

360

ctggaaaaga aaaacacca gaagaacaa aagaagaagt tactattaaa gcaaacttaa

420

tctatgcaga tggaaaaaca caaacagcag aattcaaagg aacatttgaa gaagcaacag

480

cagaagcata cagatatgca gatgcattaa agaaggacaa tggagaatat acagtagacg

540

ttgcagataa aggttatact ttaaataatta aatttgctgg aaaagaaaaa acaccagaag

600

aaccaaaga agaagttact attaaagcaa acttaatcta tgcagatgga aaaacacaaa

660

cagcagaatt caaaggaaca tttgaagaag caacagcaga agcatacaga tatgctgact

720

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tattagcagc aaaagaaaat ggtaaatata cagtagacgt tgcagataaa ggttatactt 780
taaatattaa atttgctgga aaagaaaaaa caccagaaga accaaaagaa gaagttacta 840
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ttgcagaagc aacagcagaa gcatacagat acgctgactt attagcaaaa gaaadtggta 960
aatatacagc agacttagaa gatggtggat acactattaa tattagattt gcaggtaaga 1020
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<210> 12

<211> 467

<212> PRT

<213> Artificial sequence

<220>

<223> pUC19-cell-ProtL-cexNG-HDEL fusion encoded product

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Met Ala Arg Lys Ser Leu Ile Phe Pro Val Ile Leu Leu Ala Val Leu
1           5           10          15

```

```

Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala
20          25          30

```

```

Leu Arg Lys Ser Arg Met Ala Ala Val Glu Asn Lys Glu Glu Thr Pro
35          40          45

```

```

Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val Thr Ile Lys Ala Asn
50          55          60

```

```

Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala Glu Phe Lys Gly Thr
65          70          75          80

```

```

Phe Glu Lys Ala Thr Ser Glu Ala Tyr Glu Tyr Ala Asp Thr Leu Lys
85          90          95

```

```

Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr
100         105         110

```

```

Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys
115        120        125

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Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr  
 130 135 140

Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala  
 145 150 155 160

Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val  
 165 170 175

Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys  
 180 185 190

Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn  
 195 200 205

Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr  
 210 215 220

Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala  
 225 230 235 240

Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
 245 250 255

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro  
 260 265 270

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys  
 275 280 285

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu  
 290 295 300

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr  
 305 310 315 320

Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly  
 325 330 335

Lys Lys Val Asp Glu Lys Pro Glu Gly Ile Pro Pro Thr Pro Thr Pro  
 340 345 350

Thr Ser Ala Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val Asn  
 355 360 365

Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr Gly  
 370 375 380

Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser Gly  
 385 390 395 400

Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly Ser  
 405 410 415

Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala Gly

420

425

430

Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn Ala  
 435 440 445

Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly His  
 450 455 460

Asp Glu Leu  
 465

<210> 13

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 13  
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25

<210> 14

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 14  
 cttaaagttc atcatga

17

<210> 15

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 15  
 aaaacccggg atggcgcgaa aatc

24

<210> 16

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 16

aaaagacgtc ttacggagag cgtcgcgcta atc

33

<210> 17

<211> 1560

<212> DNA

<213> Artificial sequence

<220>

<223> pBS-Sig-cex-Fx-HDEL fusion construct

<400> 17

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taagacgtcc ggtccagccg gctgccaggt tctgtggggg gtaaccagt ggaacaccgg	180
tttcaccgct caggttaccg ttaaaaacac gggctcagct ccggttgacg gttggaccct	240
gaccttctct ttccctcgg gtcagcaggt aactcaggct tggatcatcta cagttacca	300
gtctggatcc gctgttacag ttcgtaacgc tccgtggaac ggtaatatc ctgcaggtag	360
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ccacgagaag ggccggcagt ccaccaggct caagatgctg gaggtgccct acgtggaccg	1260
caacagctgc aagctgtcca gcagcttcat catcaccag aacatgttct gtgccggcta	1320



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 gaagtacggg atctacacca aggtcaccgc cttcctcaag tggatcgaca ggtccatgaa 1500  
 aaccaggggc ttgcccaagg ccaagcctac tagtcatgat gaactttaag agtccagct 1560

<210> 18

<211> 509

<212> PRT

<213> Artificial sequence

<220>

<223> pBS-Sig-cex-Fx-HDEL fusion encoded product

<400> 18

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Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala  
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Leu Arg Lys Thr Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val  
 35 40 45

Asn Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr  
 50 55 60

Gly Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser  
 65 70 75 80

Gly Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly  
 85 90 95

Ser Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala  
 100 105 110

Gly Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn  
 115 120 125

Ala Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly  
 130 135 140

Pro Thr Thr Ser Pro Thr Thr Arg Lys Leu Cys Ser Leu Asp Asn Gly  
 145 150 155 160

Asp Cys Asp Gln Phe Cys His Glu Glu Gln Asn Ser Val Val Cys Ser  
 165 170 175

Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn Gly Lys Ala Cys Ile Pro  
 180 185 190

Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr Leu Glu Arg Arg Lys Arg  
 195 200 205  
 Ser Val Ala Gln Ala Thr Ser Ser Ser Gly Glu Ala Pro Asp Ser Ile  
 210 215 220  
 Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu Asp Pro Thr Glu Asn Pro  
 225 230 235 240  
 Phe Asp Leu Leu Asp Phe Asp Gln Thr Gln Pro Glu Arg Gly Asp Asn  
 245 250 255  
 Asn Ile Glu Gly Arg Ile Val Gly Gly Gln Glu Cys Lys Asp Gly Glu  
 260 265 270  
 Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu Asn Glu Gly Phe Cys  
 275 280 285  
 Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu Thr Ala Ala His Cys  
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 Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg Asn Thr  
 305 310 315 320  
 Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val Val Ile  
 325 330 335  
 Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp Phe Asp Ile Ala Val  
 340 345 350  
 Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met Asn Val Ala Pro Ala  
 355 360 365  
 Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr Gln Lys  
 370 375 380  
 Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His Glu Lys Gly Arg Gln  
 385 390 395 400  
 Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg Asn Ser  
 405 410 415  
 Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln Asn Met Phe Cys Ala  
 420 425 430  
 Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 435 440 445  
 Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly Ile Val  
 450 455 460  
 Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys Tyr Gly Ile Tyr Thr  
 465 470 475 480  
 Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg Ser Met Lys Thr Arg

485

490

495

Gly Leu Pro Lys Ala Lys Pro Thr Ser His Asp Glu Leu  
 500 505

&lt;210&gt; 19

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Single strand DNA oligonucleotide

&lt;400&gt; 19

aaaagacgctc ggctagcggg ataattggtag cg

32

&lt;210&gt; 20

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Single strand DNA oligonucleotide

&lt;400&gt; 20

aaaaacgcgt tggggatggg gtcggac

27

&lt;210&gt; 21

&lt;211&gt; 1860

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; pBS-Sig-Tma-Fx-HDEL fusion construst

&lt;400&gt; 21

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cgttcttctc ttctctccgc cgatttactc cgccggtcac gattaccgcg acgctctccg 120

taagacgtcg gctagcggaa taatggtagc gacagcaaaa tacggaacac cggtcacgca 180

tggagagata gacgagatct ggaacacgac agaggagata gagacgaaag cggtgccat 240

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gtacgtactt gcaatcgtga aagaccccggt tctgaacaaa gacaacagca acccggtggga 360

acaggattcc gtggagatct tcatcgacga gaacaaccac aagacaggat actacgaaga 420

cgacgacgca cagttcagggt tgaactacat gaacgagcag acgtttggaa cgggaggaag 480

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caacagctgg agagatcctt caaagttcgg taacctcagg ctcatcaagg gatctggtcc 720
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<210> 22

<211> 597

<212> PRT

<213> Artificial sequence

<220>

<223> pBS-Sig-Tma-Fx-HDEL fusion encoded product

<400> 22

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Met Ala Arg Lys Ser Leu Ile Phe Pro Val Ile Leu Leu Ala Val Leu
1           5           10          15

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Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala
          20          25          30

```

```

Leu Arg Lys Thr Ser Ala Ser Gly Ile Met Val Ala Thr Ala Lys Tyr

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35                      40                      45  
 Gly Thr Pro Val Ile Asp Gly Glu Ile Asp Glu Ile Trp Asn Thr Thr  
 50                      55                      60  
 Glu Glu Ile Glu Thr Lys Ala Val Ala Met Gly Ser Leu Asp Lys Asn  
 65                      70                      75                      80  
 Ala Thr Ala Lys Val Arg Val Leu Trp Asp Glu Asn Tyr Leu Tyr Val  
 85                      90                      95  
 Leu Ala Ile Val Lys Asp Pro Val Leu Asn Lys Asp Asn Ser Asn Pro  
 100                      105                      110  
 Trp Glu Gln Asp Ser Val Glu Ile Phe Ile Asp Glu Asn Asn His Lys  
 115                      120                      125  
 Thr Gly Tyr Tyr Glu Asp Asp Asp Ala Gln Phe Arg Val Asn Tyr Met  
 130                      135                      140  
 Asn Glu Gln Thr Phe Gly Thr Gly Gly Ser Pro Ala Arg Phe Lys Thr  
 145                      150                      155                      160  
 Ala Val Lys Leu Ile Glu Gly Gly Tyr Ile Val Glu Ala Ala Ile Lys  
 165                      170                      175  
 Trp Lys Thr Ile Lys Pro Thr Pro Asn Thr Val Ile Gly Phe Asn Ile  
 180                      185                      190  
 Gln Val Asn Asp Ala Asn Glu Lys Gly Gln Arg Val Gly Ile Ile Ser  
 195                      200                      205  
 Trp Ser Asp Pro Thr Asn Asn Ser Trp Arg Asp Pro Ser Lys Phe Gly  
 210                      215                      220  
 Asn Leu Arg Leu Ile Lys Gly Ser Gly Pro Thr Pro Ser Pro Thr Arg  
 225                      230                      235                      240  
 Lys Leu Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu  
 245                      250                      255  
 Glu Gln Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala  
 260                      265                      270  
 Asp Asn Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys  
 275                      280                      285  
 Gln Thr Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser  
 290                      295                      300  
 Ser Gly Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala  
 305                      310                      315                      320  
 Asp Leu Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asp Gln  
 325                      330                      335

Thr Gln Pro Glu Arg Gly Asp Asn Asn Ile Glu Gly Arg Ile Val Gly  
340 345 350

Gly Gln Glu Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile  
355 360 365

Asn Glu Glu Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe  
370 375 380

Tyr Ile Leu Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys  
385 390 395 400

Val Arg Val Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala  
405 410 415

Val His Glu Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu  
420 425 430

Thr Tyr Asp Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr  
435 440 445

Phe Arg Met Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala  
450 455 460

Glu Ser Thr Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly  
465 470 475 480

Arg Thr His Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu  
485 490 495

Val Pro Tyr Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile  
500 505 510

Ile Thr Gln Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp  
515 520 525

Ala Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp  
530 535 540

Thr Tyr Phe Val Thr Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg  
545 550 555 560

Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp  
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Ile Asp Arg Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Pro Thr  
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Ser His Asp Glu Leu  
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